

Probable histone H2A.4 (Os05g0461400, LOC_Os05g38640), Recombinant Protein

Cat RP14155

Size 0.02 mg (E-Coli)/ 0.1 mg (E-Coli)/ 0.02 mg (Yeast)/ 0.1 mg
(Yeast)/ 0.02 mg (Baculovirus)/ 0.02 mg (Mammalian-Cell)/ 1

mg (E-Coli)/ 0.1 mg (Baculovirus)/ 1 mg (Yeast)/ 0.1 mg
(Mammalian-Cell)/ 1 mg (Baculovirus)/ 0.5 mg (Mammalian-
Oryza sativa subsp. japonica (Rice)
Cell)

Species

Full Product Name

Recombinant Oryza sativa subsp. japonica Probable histone H2A.4 (Os05g0461400, LOC_Os05g38640)

Product Gene Name

Os05g0461400 recombinant protein

Product Synonym Gene Name

Os05g0461400; LOC_Os05g38640

Purity

Greater or equal to 85% purity as determined by SDS-PAGE. (lot specific)

Sequence

MEVGAKVPPK AGAGGRRGGG GPKKKPVSRV VKAGLQFPVG RIGRYLKQGR YSQRIGTGAP VYLAADVLEYL
AAEVLELAGN AARDNKKNR IPRHVLLAIR NDEELGKLLA GVTIAHGGVL PNINPVLLPK KTGSAAAKEA
KEGKTPKSPK KATTKSPKKA AAA

Sequence Positions

1-163, Full length protein

Format

Lyophilized or liquid (Format to be determined during the manufacturing process)

Host

E Coli or Yeast or Baculovirus or Mammalian Cell

Molecular Weight

16,971 Da

Storage

Store at -20°C. For long-term storage, store at -20°C or -80°C. Store working aliquots at 4°C for up to one week.
Repeated freezing and thawing is not recommended.

NCBI Accession

XP_015640099.1

NCBI GI

1002271530

NCBI GenBank Nucleotide

XM_015784613.1

NCBI GeneID

4339022

FOR RESEARCH OR FURTHER MANUFACTURING USE ONLY

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NCBI Official Full Name
probable histone H2A.4

NCBI Official Symbol

LOC4339022

NCBI Official Synonym Symbols

OsJ_018061; OJ1525_A02.1; OJ1281_H05.14

NCBI Protein Information

probable histone H2A.4

UniProt Gene Name

Os05g0461400

UniProt Protein Name

Probable histone H2A.4

UniProt Primary Accession

Q6L500

UniProt Secondary Accession

Q0DHJ7; B7EDG0

UniProt Related Accession

Q6L500

UniProt Comments

Core component of nucleosome. Nucleosomes wrap and compact DNA into chromatin, limiting DNA accessibility to the cellular machineries which require DNA as a template. Histones thereby play a central role in transcription regulation, DNA repair, DNA replication and chromosomal stability. DNA accessibility is regulated via a complex set of post-translational modifications of histones, also called histone code, and nucleosome remodeling.

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